

SEQ ID No 1. - HCV Core Protein

GTGCCCCTTCAGCCTACCAAGTGCGCAAC 930
CACGGGCGAAGTCGGATGGTTCACGCGTTG
V P A S A Y Q V R N 196

SECRET

SEQ ID No 2. - HCV Core Protein - Amino acids 125 to 144

ACCCTTACGTGCGGCTTCGTTCGATCTCATGGGGTACATACCGCTCGTCGGCGCCCCCTCTT 777
TGGGAATGCACGCCGAAGCAGCTAGAGTACCCCATGTATGGCGAGCAGCCGCGGGGAGAA
T L T C G F V D L M G Y I P L V G A P L 144

SEQ ID No 3. - HCV Core Protein - Amino acids 161 to 166

GGTGTGAACATATGCAACA 840
CCACACTTGATACGTTGT
G V N Y A T 166

SEQ ID No.4 - human ADRP - nucleotide sequence

CGTCTTCGGGACGCGCCCGCTCTTCGCCTTTCGCTGCAGTCCGTCGATTTCTTTCTCCAG 60
GAAGAAAAATGGCATCCGTTGCAGTTGATCCACAACCGAGTGTGGTGACTCGGGTGGTCA 120
ACCTGCCCTTGGTGAGCTCCACGTATGACCTCATGTCCTCAGCCTATCTCAGTACAAAGG 180
ACCAGTATCCCTACCTGAAGTCTGTGTGTGAGATGSCAGAGAACGGTGTGAAGACCATCA 240
CCTCCGTGGCCATGACCAGTGCTCTGCCCATCATCCAGAAGCTAGAGCCGCAAATTGCAG 300
TTGCCGATACCTATGCCTGTAAGGGGCTAGACAGGATTGAGGAGAGACTGCCTATTCTGA 360
ATCAGCCATCAACTCAGATTGTTGCCAATGCCAAAGGCGCTGTGACTGGGGCAAAGATG 420
CTGTGACGACTACTGTGACTGGGGCCAAGGATTCTGTNGCCAGCACGATCACAGGGGTGA 480
TGGACAAGACCAAAGGGGCAGTGACTGGCAGTGTGGAGAAGACCAAGTCTGTGGTCAGTG 540
GCAGCATTAACACAGTCTTGGGGAGTCGGATGATGCAGCTCGTGAGCAGTGGCGTAGAAA 600
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TTAGACTGGGATCCCTGTCTACCAAGCTTCACTCCCGTGCCTACCAGCAGGCTCTCAGCA 780
GGGTAAAGAAGCTAAGCAAAAAAGCCAACAGACCATTCTCAGCTCCATTCTACTGTTC 840
ACCTGATTGAATTTGCCAGGAAGAATGTGTATAGTGCCAATCAGAAAATTGAGGATGCTC 900
AGGATAAGCTCTACCTCTCATGGGTAGAGTGGAAAAGGAGCATTGGATATGATGATACTG 960
ATGAGTCCCCTGTGCTGAGCACATTGAGTCACGTACTCTTGCAATTGCCCGCAACCTGA 1020
CTCAGCAGCTCCAGACCACGTGCCACACCCTCCTGTCCAACATCCAAGGTGTACCACAGA 1080
ACATCCAAGATCAAGCCAAGCACATGGGGGTGATGGCAGGCGACATCTACTCAGTGTTCC 1140
GCAATGCTGCCTCCTTTAAAGAAGTGTCTGACAGCCTCCTCACTTCTAGCAAGGGGCAGC 1200
TGCAGAAAATGAAGGAATCTTTAGATGACGTGATGGATTATCTTGTTAACAACACGCCCC 1260
TCAACTGGCTGGTAGGTCCCTTTTATCCTCAGCTGACTGAGTCTCAGAATGCTCAGGACC 1320

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ValAsnLeuProLeuValSerSerThrTyrAspLeuMetSerSerAla	32
TyrLeuSerThrLysAspGlnTyrProTyrLeuLysSerValCysGlu	48
MetXaaGluAsnGlyValLysThrIleThrSerValAlaMetThrSer	64
AlaLeuProIleIleGlnLysLeuGluProGlnIleAlaValAlaAsp	80
ThrTyrAlaCysLysGlyLeuAspArgIleGluGluArgLeuProIle	96
LeuAsnGlnProSerThrGlnIleValAlaAsnAlaLysGlyAlaVal	112
ThrGlyAlaLysAspAlaValThrThrThrValThrGlyAlaLysAsp	128
SerValAlaSerThrIleThrGlyValMetAspLysThrLysGlyAla	144
ValThrGlySerValGluLysThrLysSerValValSerGlySerIle	160
AsnThrValLeuGlySerArgMetMetGlnLeuValSerSerGlyVal	176
GluAsnAlaLeuThrLysSerGluLeuLeuValGluGlnTyrLeuPro	192
LeuThrGluGluGluLeuGluLysGluAlaLysLysValGluGlyPhe	208
AspLeuValGlnLysProSerTyrTyrValArgLeuGlySerLeuSer	224
ThrLysLeuHisSerArgAlaTyrGlnGlnAlaLeuSerArgValLys	240
GluAlaLysGlnLysSerGlnGlnThrIleSerGlnLeuHisSerThr	256
ValHisLeuIleGluPheAlaArgLysAsnValTyrSerAlaAsnGln	272
LysIleGlnAspAlaGlnAspLysLeuTyrLeuSerTrpValGluTrp	288
LysArgSerIleGlyTyrAspAspThrAspGluSerHisCysAlaGlu	304
HisIleGluSerArgThrLeuAlaIleAlaArgAsnLeuThrGlnGln	320

LeuGlnThrThrCysHisThrLeuLeuSerAsnIleGlnGlyValPro	336
GlnAsnIleGlnAspGlnAlaLysHisMetGlyValMetAlaGlyAsp	352
IleTyrSerValPheArgAsnAlaAlaSerPheLysGluValSerAsp	368
SerLeuLeuThrSerSerLysGlyGlnLeuGlnLysMetLysGluSer	384
LeuAspAspValMetAspTyrLeuValAsnAsnThrProLeuAsnTrp	400
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AspGlnGlyAlaGluMetAspLysSerSerGlnGluThrGlnArgSer	432
GluHisLysThrHis	437

[illegible]